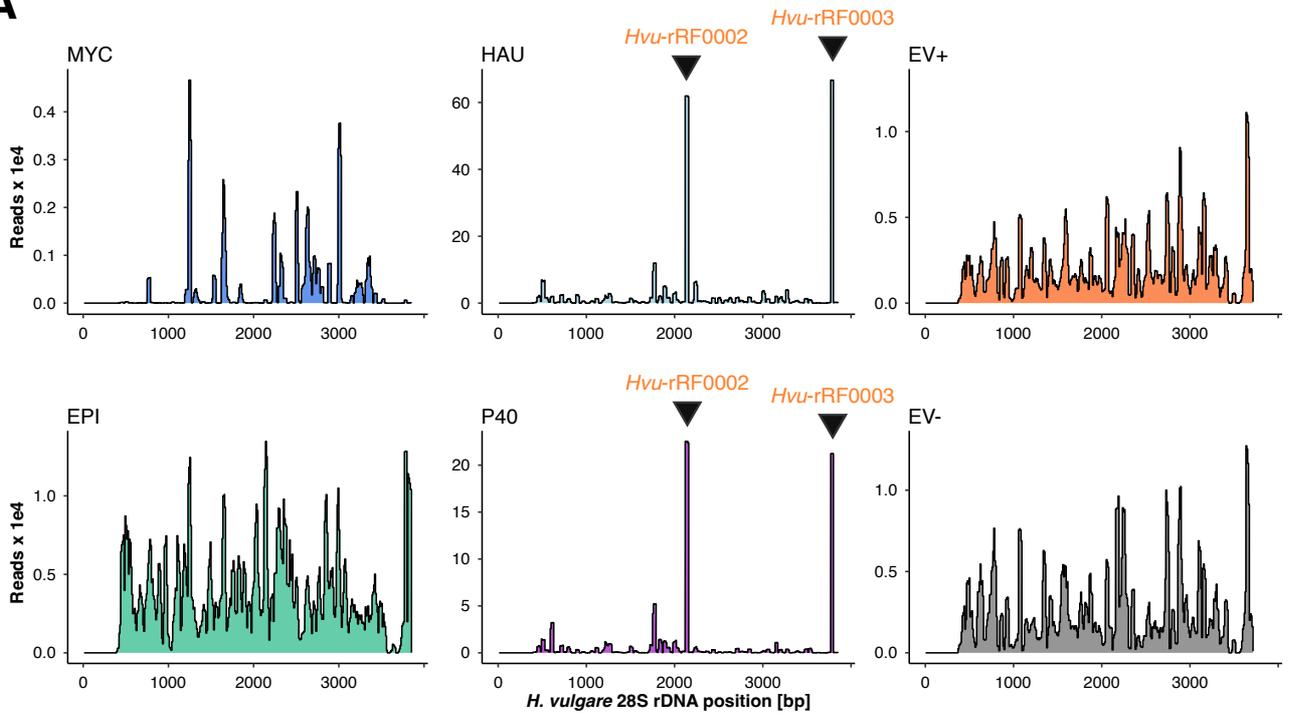
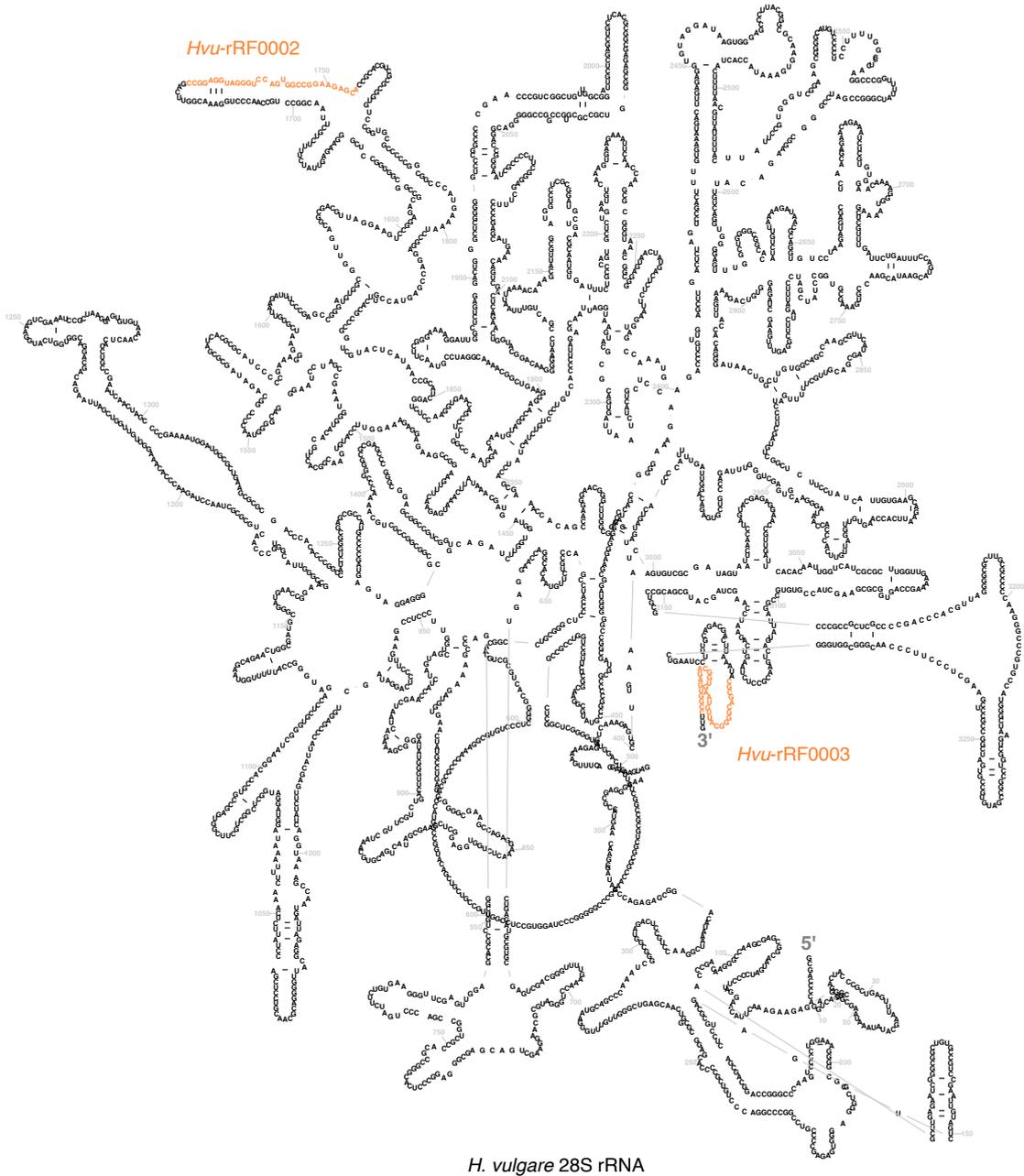


A**B***H. vulgare* 28S rRNA

Supplementary Figure 4. Specific barley 28S rRNA-derived sRNAs are enriched in the 31-33 base long reads. (A) We aligned sRNA sequencing reads of 31-33 bases in length to the *H. vulgare* 28S rDNA (3,853 bases in length). The graphs display the number of reads identified (y-axis) mapping to each position of the barley 28S rDNA (x-axis). Epiphytic fungal mycelium (MYC), infected epidermis without mycelium (EPI), fungal haustoria (HAU), microsomes of the epidermis without haustoria (P40), apoplastic extracellular vesicles (EV+), and apoplastic extracellular vesicles of non-infected control plants (EV-). (B) Secondary structure of the 28S rRNA of *H. vulgare* (RFAM accession CAJW010993076.1:203-48; RNA central accession URS000212856A_112509) predicted by R2DT in RNA central (<https://rnacentral.org>). The sequence stretches shown in orange indicate the over-represented 28S rRNA fragments *Hvu*-rRF0002 and *Hvu*-rRF0003 from the HAU and P40 samples.